WHAT IS CLAIMED IS:

1. A gene assay method comprising the steps of:

detecting a mutation of at least one base in the coding region of an optineurin(OPTN) gene of a human subject; and predicting future onset of glaucoma in the subject using the mutation as an index.

2. The gene assay method of claim 1, wherein the coding region of said glaucoma-related gene is an OPTN gene has a nucleic acid sequence denoted by SEQ ID NO: 1.

3. The gene assay method of claim 2, wherein said mutation is a substitution of G for A at position 619 and/or a substitution of A for G at position 898 in the nucleic acid sequence denoted by SEQ ID NO:1.

4. The gene assay method of claim 2, wherein said mutation is a deletion of one or more bases in the nucleic acid sequence denoted by SEQ ID NO: 1.

5. The gene assay method of claim 2, wherein said mutation is an insertion of one or more bases in the nucleic acid sequence denoted by SEQ ID NO: 1.

6. The gene assay method of claim 2, wherein said mutation is two or more substitutions of bases in the nucleic acid sequence denoted by SEQ ID NO: 1.

7. The gene assay method according to claim 1, wherein the glaucoma is primary open angle glaucoma and/or normal ocular tension glaucoma.

8. The gene assay method according to claim 1, wherein the mutation is detected by using an oligonucleotide capable of forming a hybrid at a specific position of the coding region of the OPTN gene.

9. An oligonucleotide selected from the group consisting of oligonucleotides comprising sequences as follows:

(1) an oligonucleotide consisting of a base sequence represented by any of SEQ ID NOs: 15 to 40;

(2) a complementary chain of an oligonucleotide according to (1);

(3) an oligonucleotide that hybridizes with an oligonucleotide according to (1) or (2) under stringent conditions;

(4) an oligonucleotide having a homology of 60% or more to an oligonucleotide according to any one of (1) to (3); and

(5) an oligonucleotide according to any one of (1) to (4) having one to several bases mutated by substitution, deletion, insertion or addition.

10. A gene assay method for predicting future onset of primary open angle glaucoma and/or normal ocular tension glaucoma, comprising the steps of:

(a) isolating a polynucleotide sample from a subject suspected of having a mutation in a glaucoma-related gene,

(b) performing a nucleic acid amplification process on said polynucleotide using at least one oligonucleotide selected from the group consisting of oligonucleotides comprising sequences as follows:

(1) an oligonucleotide consisting of a base sequence represented by any of SEQ ID NOs: 15 to 40;

(2) a complementary chain of an oligonucleotide according to (1);

(3) an oligonucleotide that hybridizes with an oligonucleotide according to (1) or (2) under stringent conditions;

(4) an oligonucleotide having a homology of 60% or more to an oligonucleotide according to any one of (1) to (3) ; and

(5) an oligonucleotide according to any one of (1) to (4) having one to several bases mutated by substitution, deletion, insertion or addition

(c) detecting a mutation of at least one base in the coding region of a glaucoma-related gene; and

(d) predicting future onset of primary open angle glaucoma and/or normal ocular tension glaucoma using the mutation as an index.

11. An assaying reagent or an assaying reagent kit comprising an oligonucleotide of claim 9.